

SEQUENCE LISTING

<110> Hua, Shao-bing
Pauling, Michelle H.
Zhu, Li

<120> HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEFICIENCY VIRUS

<130> 25636-718

<160> 54

<170> PatentIn version 3.1

<210> 1

<211> 352

<212> PRT

<213> Homo sapiens

<400> 1

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
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Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20 25 30

Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
35 40 45

Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
50 55 60

Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
65 70 75 80

Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
85 90 95

Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100 105 110

Genetastix.718.ST25

Phe	Ser	Gly	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	Ile	Asp	Arg	Tyr	Leu
		115					120					125			
Ala	Val	Val	His	Ala	Val	Phe	Ala	Leu	Lys	Ala	Arg	Thr	Val	Thr	Phe
	130					135					140				
Gly	Val	Val	Thr	Ser	Val	Ile	Thr	Trp	Val	Val	Ala	Val	Phe	Ala	Ser
145					150					155					160
Leu	Pro	Gly	Ile	Ile	Phe	Thr	Arg	Ser	Gln	Lys	Glu	Gly	Leu	His	Tyr
				165					170					175	
Thr	Cys	Ser	Ser	His	Phe	Pro	Tyr	Ser	Gln	Tyr	Gln	Phe	Trp	Lys	Asn
			180					185					190		
Phe	Gln	Thr	Leu	Lys	Ile	Val	Ile	Leu	Gly	Leu	Val	Leu	Pro	Leu	Leu
		195					200					205			
Val	Met	Val	Ile	Cys	Tyr	Ser	Gly	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Cys
	210					215					220				
Arg	Asn	Glu	Lys	Lys	Arg	His	Arg	Ala	Val	Arg	Leu	Ile	Phe	Thr	Ile
225					230					235					240
Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp	Ala	Pro	Tyr	Asn	Ile	Val	Leu	Leu
				245					250					255	
Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe	Gly	Leu	Asn	Asn	Cys	Ser	Ser	Ser
			260					265					270		
Asn	Arg	Leu	Asp	Gln	Ala	Met	Gln	Val	Thr	Glu	Thr	Leu	Gly	Met	Thr
		275					280					285			
His	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Val	Gly	Glu	Lys	Phe
	290					295					300				

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Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
305 310 315 320

Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
340 345 350

<210> 2
<211> 17
<212> PRT
<213> Homo sapiens
<400> 2

Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp
1 5 10 15

Gln

<210> 3
<211> 29
<212> PRT
<213> Homo sapiens

<400> 3

Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln
1 5 10 15

Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr His Cys
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<210> 4
<211> 20
<212> PRT
<213> Artificial Sequence

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<220>
<223>  G4S Linker

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1          5          10          15

Gly Gly Gly Ser
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<210>  5
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  DNA of G4S Linker

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<210>  6
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  5' Homologous Sequence

<400>  6
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<210>  7
<211>  57
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  3' Homologous Sequence

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Genetastix.718.ST25

<400> 7

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<210> 8

<211> 36

<212> PRT

<213> Homo sapiens

<400> 8

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
1 5 10 15

Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20 25 30

Leu Pro Pro Leu
35

<210> 9

<211> 32

<212> PRT

<213> Homo sapiens

<400> 9

Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe
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Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile
20 25 30

<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 10

ggagaattcg attatcaagt gtcaagtcca
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<210> 11
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

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cgcggtatcct tagagcggag gcaggaggcg g
31

<210> 12
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
ggagaattca ccagatctca aaaagaagg
29

<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
cgcggtatcct tatatcttta atgtctggaa att
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<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

Genetastix.718.ST25

<220>

<223> Primer

<400> 14

caggaattct ttggcctgaa t
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<210> 15

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 15

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<210> 16

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Clone 15.186.35

<400> 16

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acctgcacct tgtctggggt ctcactcagc actagtggag tgagtgtggg ctggatccgt
120

cagccccag gaaaggccct tgagtggctt gcaagcataa attggaatga tgataagtgc
180

tacagcccat ctctgaaaag caggctcacc atcaccaagg acacccccaa aaaccagggtg
240

gtccttgcaa tgagcaacat ggaccctgcg gacacagcca catattcctg tgcactcgat
300

t t tttgatggtt ctgatatctg gggcccaggg

acaatgggtca ccgtctcttc aggcgggtggt ggatcaggcg gcggaggatc tggcggagggt
420

ggcagcgggtg gtggaggcag ttcctatgag ctgatgcagc taccctcagt gtccgtgtcc
480

ccaggacaga cagccagcat cacctgctct ggagataatt tgggggataa atatgcctgc
540

tggtatcaac agaagccagg ccggtccccct gtgctgggtca tttatggaga taacaagcgg
600

ccctcaggga tccctgagcg attctctggc tccaactctg ggaacacagc cactctgacc
660

atcagcggga cccaggctat ggatgaggct gactattact gtcaggcgtg ggacaccagc
720

actgctgtct tcggaactgg gaccaagctc accgtccta
759

<210> 17

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> Clone 15.186.35

<400> 17

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Thr	Leu	Thr	Leu	Thr	Cys	Thr	Leu	Ser	Gly	Phe	Ser	Leu	Ser	Thr	Ser
			20					25					30		

Gly	Val	Ser	Val	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Ala	Leu	Glu
		35					40					45			

Trp	Leu	Ala	Ser	Ile	Asn	Trp	Asn	Asp	Asp	Lys	Cys	Tyr	Ser	Pro	Ser
	50					55					60				

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Leu	Lys	Ser	Arg	Leu	Thr	Ile	Thr	Lys	Asp	Thr	Pro	Lys	Asn	Gln	Val
65					70					75					80
Val	Leu	Ala	Met	Ser	Asn	Met	Asp	Pro	Ala	Asp	Thr	Ala	Thr	Tyr	Ser
				85					90					95	
Cys	Ala	Leu	Asp	Met	Pro	Pro	His	Asp	Ser	Gly	Pro	Gln	Ser	Phe	Asp
			100					105					110		
Ala	Ser	Asp	Val	Trp	Gly	Pro	Gly	Thr	Met	Val	Thr	Val	Ser	Ser	Gly
		115					120					125			
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
	130					135					140				
Gly	Gly	Ser	Ser	Tyr	Glu	Leu	Met	Gln	Leu	Pro	Ser	Val	Ser	Val	Ser
145					150					155					160
Pro	Gly	Gln	Thr	Ala	Ser	Ile	Thr	Cys	Ser	Gly	Asp	Asn	Leu	Gly	Asp
				165					170					175	
Lys	Tyr	Ala	Cys	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Arg	Ser	Pro	Val	Leu
			180					185					190		
Val	Ile	Tyr	Gly	Asp	Asn	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe
		195					200					205			
Ser	Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Thr
	210					215					220				
Gln	Ala	Met	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ala	Trp	Asp	Thr	Ser
225					230					235					240
Thr	Ala	Val	Phe	Gly	Thr	Gly	Thr	Lys	Leu	Thr	Val	Leu			
				245					250						

Genetastix.718.ST25

<210> 18
 <211> 762
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Clone 15.150.11

<400> 18
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acttgcaactg tctctggtgg ctccatcggc catgactact ggagctggat acggcagccc
 120

ccaggggagg gactggagtg gattgggttc atcttcttcg atgggagcac caactacaac
 180

ccctccctca acggtcgagt caccatctca ctgcacacgt cgaagaatca gctctccctg
 240

aggctgacct ctgtgaccgc tgcggacacg gccgtgtatt tctgtgagag actaaagggg
 300

gcgtgggttat tgtctgaacc cccttacttc agctccgacg gcatggacgt ctggggccaa
 360

gggaccacgg tcaccgtccc ctcaggcggc ggtggatcag gcggcggagg atctggcggg
 420

ggtggcagcg gtggtggagg cagtaatttt atgctgactc agccccctc agcgtctggg
 480

acccccgggc agagggtcag catctcttgt tctgggagca gctccgacat cggaagtaat
 540

actgtaaact ggtaccagca actcccagga acggccccca aactcctcat ctatagtaat
 600

aatcagcggc cctcaggggt ccctgaccga ttctctggct tcaagtctgg cacctcagcc
 660

tccctgggtca tcagtggcct ccagtctgag gatgaggctg attattattg tgcagcatgg
 720

gatgagagcc tgaatggtgt ggtgttcggc ggaggaccaa gg
 762

Genetastix.718.ST25

<210> 19
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Clone 15.150.11

<400> 19

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	1	5	10	15
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Gly	His	Asp	20	25	30	
Tyr	Trp	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Glu	Gly	Leu	Glu	Trp	Ile	35	40	45	
Gly	Phe	Ile	Phe	Phe	Asp	Gly	Ser	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Asn	50	55	60	
Gly	Arg	Val	Thr	Ile	Ser	Leu	Asp	Thr	Ser	Lys	Asn	Gln	Leu	Ser	Leu	65	70	75	80
Arg	Leu	Thr	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Phe	Cys	Ala	85	90	95	
Arg	Leu	Lys	Gly	Ala	Trp	Leu	Leu	Ser	Glu	Pro	Pro	Tyr	Phe	Ser	Ser	100	105	110	
Asp	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Pro	Ser	115	120	125	
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	130	135	140	
Gly	Gly	Gly	Ser	Asn	Phe	Met	Leu	Thr	Gln	Pro	Pro	Ser	Ala	Ser	Gly				

Genetastix.718.ST25

145 150 155 160

Thr Pro Gly Gln Arg Val Ser Ile Ser Cys Ser Gly Ser Ser Ser Asp
165 170 175

Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
180 185 190

Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro
195 200 205

Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser Leu Val Ile
210 215 220

Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp
225 230 235 240

Asp Glu Ser Leu Asn Gly Val Val Phe Gly Gly Gly Pro Arg
245 250

<210> 20
<211> 750
<212> DNA
<213> Artificial Sequence

<220>
<223> Clone 15.150.12

<400> 20
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acctgcgctg tctctgggtgc gtcgttttagt ggttattatt ggagctggat ccgccagccc
120

ccagggaagg ggctggagtg gattggggag atcaatcatc gtggaagcac tacctacaac
180

ccgtccctcg acggtcgagt caccatatca ttagacacat ctaccaacca gatctccctt
240

Genetastix.718.ST25

aaactgacct ctatgaccgc cgcggaacacg gccgtgtatt actgtgacgag gacagtggct
300

ggtactagtg actactgggg ccaggggaacc ctggtcaccg tttcctcagg gagtgcaccc
360

gccccaacgg gcggtgggtg atcaggcggc ggaggatctg gcggagggtg cagcgggtgg
420

ggaggcagta aaacgacact cacgcagtct ccagcattca tgtcagcgcac tccaggagac
480

aaagtcagca tctcctgcaa agccagccga gacgttgatg atgatgtgaa ctggtaccaa
540

cagagaccag gagaagctcc tatttttcatt attgaagatg ctactactct cgttcctgga
600

atctcacctc gattcagtgg cagcgggtat ggaaccgatt ttaccctcac aattaataac
660

atcgattctg aggatgctgc atattatttc tgtctacaac atgataattt cccgctcacc
720

ttcggcggag ggaccaaggt ggagatcaaa
750

<210> 21
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 15.150.12

<400> 21

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1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Ala Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Genetastix.718.ST25

Gly	Glu	Ile	Asn	His	Arg	Gly	Ser	Thr	Thr	Tyr	Asn	Pro	Ser	Leu	Asp
50						55					60				
Gly	Arg	Val	Thr	Ile	Ser	Leu	Asp	Thr	Ser	Thr	Asn	Gln	Ile	Ser	Leu
65					70					75					80
Lys	Leu	Thr	Ser	Met	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85					90					95	
Arg	Thr	Val	Ala	Gly	Thr	Ser	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val
			100					105					110		
Thr	Val	Ser	Ser	Gly	Ser	Ala	Ser	Ala	Pro	Thr	Gly	Gly	Gly	Gly	Ser
		115					120					125			
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Lys
	130					135					140				
Thr	Thr	Leu	Thr	Gln	Ser	Pro	Ala	Phe	Met	Ser	Ala	Thr	Pro	Gly	Asp
145					150					155					160
Lys	Val	Ser	Ile	Ser	Cys	Lys	Ala	Ser	Arg	Asp	Val	Asp	Asp	Asp	Val
				165					170					175	
Asn	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Glu	Ala	Pro	Ile	Phe	Ile	Ile	Glu
			180					185					190		
Asp	Ala	Thr	Thr	Leu	Val	Pro	Gly	Ile	Ser	Pro	Arg	Phe	Ser	Gly	Ser
		195					200					205			
Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Asn	Ile	Asp	Ser	Glu
	210					215					220				
Asp	Ala	Ala	Tyr	Tyr	Phe	Cys	Leu	Gln	His	Asp	Asn	Phe	Pro	Leu	Thr
225					230					235					240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 245 250

<210> 22
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Clone 15.150.24

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 120
 cagccccag gaaaggccct ggaatggctt gcactcattt attgggatga tgataagcgc
 180
 tacagcccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaagcagggtg
 240
 gtccttacia tgaccaacgt ggacccagcg gacacagcca cctattactg tacacacgag
 300
 caatactatt atgatactag tggtcagcca tactactttg acttctgggg ccagggcacc
 360
 ctggtcaccg tctcctcagg cgggtgggtgga tcaggcgggc gaggatctgg cggagggtggc
 420
 agcgggtggtg gaggcagtaa catccagggtg acccagtctc catcctccct gtctgcatct
 480
 gtaggagaca gagtcacat gacttgccgg gcgagtcagg acattaggaa gaatttaa
 540
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 600
 gaaacagggg tcccatcaag gttcagtggg agtggatctg ggacagattt tatcctcacc
 660

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atcagcagcc tgcagcctga agatattgca acatactact gtcaacagtc tgattattta
720

ccgctcactt tcggcggagg gaccaaagtg gatatcaaa
759

<210> 23
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 15.150.24
<400> 23

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
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20 25 30

Gly Glu Gly Val Gly Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Lys Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Thr His Glu Gln Tyr Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr
100 105 110

Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
115 120 125

Genetastix.718.ST25

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Asn Ile Gln Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
145 150 155 160

Val Gly Asp Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asp Ile Arg
165 170 175

Lys Asn Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val
180 185 190

Leu Ile Tyr Asp Ala Ser Asp Leu Glu Thr Gly Ile Pro Ser Arg Phe
195 200 205

Ser Gly Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu
210 215 220

Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Tyr Leu
225 230 235 240

Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
245 250

<210> 24
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Clone 15.186.35 Variant

<400> 24
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60

acctgcacct tgtctggggt ctcactcagc actagtggag tgagtgtggg ctggatccgt
120

Genetastix.718.ST25

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cagccccccag gaaaggccct tgagtggctt gcaagcataa attggaatga tgataagtgc
180
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240
gtccttgcaa tgagcaacat ggaccctgcg gacacagcca catattcctg tgcactcgat
300
atgccccccc atgatagtgg cccgcaatct tttgatgctt ctgatgtctg gggcccaggg
360
acaatgggtca ccgtctcttc aggcgggtggt ggatcaggcg gcggaggatc tggcggaggt
420
ggcagcgggtg gtggaggcag ttcctatgag ctgatgcagc taccctcagt gtccgtgtcc
480
ccaggacaga cagccagcat cacctgctct ggagataatt tggggggataa atatgcctgc
540
tggtatcaac agaagccagg ccggtcccct gtgctgggtca tttatggaga taacaagcgg
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ccctcaggga tccctgagcg attctctggc tccaactctg ggaacacagc cactctgacc
660
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actgctgtct tcggaactgg gaccaagctc accgtccta
759

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<210> 25
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 15.186.35 Variant

<400> 25

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Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1           5           10          15

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Genetastix.718.ST25

Thr	Leu	Thr	Leu	Thr	Cys	Thr	Leu	Ser	Gly	Phe	Ser	Leu	Ser	Thr	Ser
			20					25					30		
Gly	Val	Ser	Val	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Ala	Leu	Glu
		35					40					45			
Trp	Leu	Ala	Ser	Ile	Asn	Trp	Asn	Asp	Asp	Lys	Cys	Tyr	Ser	Pro	Ser
	50					55					60				
Leu	Lys	Ser	Arg	Leu	Thr	Ile	Thr	Lys	Asp	Thr	Pro	Lys	Asn	Gln	Val
65					70					75					80
Val	Leu	Ala	Met	Ser	Asn	Met	Asp	Pro	Ala	Asp	Thr	Ala	Thr	Tyr	Ser
				85					90					95	
Cys	Ala	Leu	Asp	Met	Pro	Pro	His	Asp	Ser	Gly	Pro	Gln	Ser	Phe	Asp
			100					105					110		
Ala	Ser	Asp	Val	Trp	Gly	Pro	Gly	Thr	Met	Val	Thr	Val	Ser	Ser	Gly
		115					120					125			
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
	130					135					140				
Gly	Gly	Ser	Ser	Tyr	Glu	Leu	Met	Gln	Leu	Pro	Ser	Val	Ser	Val	Ser
145					150					155					160
Pro	Gly	Gln	Thr	Ala	Ser	Ile	Thr	Cys	Ser	Gly	Asp	Asn	Leu	Gly	Asp
				165					170					175	
Lys	Tyr	Ala	Cys	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Arg	Ser	Pro	Val	Leu
			180					185					190		
Val	Ile	Tyr	Gly	Asp	Asn	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe
		195					200					205			

Genetastix.718.ST25

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
210 215 220

Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Thr Ser
225 230 235 240

Thr Ala Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
245 250

<210> 26

<211> 774

<212> DNA

<213> Artificial Sequence

<220>

<223> Clone 15.150.11 Variant

<400> 26

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc
60

acttgcaactg tctctgggtgg ctccatcggt catgactact ggagctggat acggcagccc
120

ccaggggagg gactggagtg gattggtttc atcttcttcg atgggagcac caactacaac
180

ccctccctca acggtcgagt caccatctca ctcgacacgt cgaagaatca gctctccctg
240

aggctgacct ctgtgaccgc tgcggacacg gccgtgtatt tctgtgagag actaaagggg
300

gcgtgggttat tgtctgaacc cccttacttc agctccgacg gcatggacgt ctggggccaa
360

gggaccacgg tcaccgtctc ctcaggcggt ggtggatcag gcggcggagg atctggcgga
420

ggtggcagcg gtggtggagg cagtaatttt atgctgactc agccccctc agcgtctggg
480

acccccgggc agagggtcag catctcttgt tctgggagca gctccgacat cggaagtaat
540

actgtaaact ggtaccagca actcccagga acggccccc aactcctcat ctatagtaat
600

aatcagcggc cctcaggggt ccctgaccga ttctctggct tcaagtctgg cacctcagcc
660

tccttggtca tcagtggcct ccagtctgag gatgaggctg attattattg tgcagcatgg
720

gatgagagcc tgaatggtgt ggtgttcggc ggaggaacca aggtgaccgt ccta
774

<210> 27
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 15.150.11

<400> 27

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly His Asp
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile
35 40 45

Gly Phe Ile Phe Phe Asp Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Leu Ser Leu
65 70 75 80

Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala
85 90 95

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser

Genetastix.718.ST25

100

105

110

Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly
145 150 155 160

Thr Pro Gly Gln Arg Val Ser Ile Ser Cys Ser Gly Ser Ser Ser Asp
165 170 175

Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
180 185 190

Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro
195 200 205

Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser Leu Val Ile
210 215 220

Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp
225 230 235 240

Asp Glu Ser Leu Asn Gly Val Val Phe Gly Gly Gly Thr Lys Val Thr
245 250 255

Val Leu

<210> 28
<211> 750
<212> DNA
<213> Artificial Sequence

Genetastix.718.ST25

<220>

<223> Clone 15.150.12 Variant

<400> 28

caggtgcagc tacagcagtg gggcgcagga ctgttgaagt cttggggaac cctgtccctc
60

acctgcgctg tctctggtgc gtcgttttagt ggttattatt ggagctggat ccgccagccc
120

ccaggggaagg ggctggagtg gattggggag atcaatcatc gtggaagcac tacctacaac
180

ccgtccctcg acggtcgagt caccatatca ttagacacat ctaccaacca gatctccctt
240

aaactgacct ctatgaccgc cgcggacacg gccgtgtatt actgtgcgag gacagtggct
300

gggtactagt actactgggg ccaggggaacc ctgggtcaccg tttcctcagg gagtgcattc
360

gccccaacgg gcggtggtgg atcaggcggc ggaggatctg gcggagggtgg cagcgggtggt
420

ggaggcagtg aaacgacact cacgcagtct ccagcattca tgtcagcgac tccaggagac
480

aaagtcagca tctcctgcaa agccagccga gacgttgatg atgatgtgaa ctggtaccaa
540

cagagaccag gagaagctcc tattttcatt attgaagatg ctactactct cgttcctgga
600

atctcacctc gattcagtgg cagcgggtat ggaaccgatt ttaccctcac aattaataac
660

atcgattctg aggatgctgc atattatttc tgtctacaac atgataattt cccgctcacc
720

ttcggcggag ggaccaaggt ggagatcaaa
750

<210> 29

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<223> Clone 15.150.12 Variant

<400> 29

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Ser Trp Gly
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Ala Ser Phe Ser Gly Tyr
 20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Glu Ile Asn His Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Asp
 50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Thr Asn Gln Ile Ser Leu
 65 70 75 80

Lys Leu Thr Ser Met Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Thr Val Ala Gly Thr Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Gly Ser Ala Ser Ala Pro Thr Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
 130 135 140

Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly Asp
 145 150 155 160

Lys Val Ser Ile Ser Cys Lys Ala Ser Arg Asp Val Asp Asp Asp Val
 165 170 175

Asn Trp Tyr Gln Gln Arg Pro Gly Glu Ala Pro Ile Phe Ile Ile Glu
 180 185 190

Asp Ala Thr Thr Leu Val Pro Gly Ile Ser Pro Arg Phe Ser Gly Ser
 195 200 205

Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Asp Ser Glu
 210 215 220

Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Asn Phe Pro Leu Thr
 225 230 235 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 245 250

<210> 30
 <211> 759
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Clone 15.150.24 Variant

<400> 30
 caggtcacct tgaaggagtc tggctcctacg ctgggtgaaac ccacacagac cctcacgctg
 60

acctgcacct tctctggggt ctcactcaga actactggag aggggtgtggg ctgggtccgt
 120

cagccccag gaaaggccct ggaatggctt gcactcattt attgggatga tgataagcgc
 180

tacagcccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaagcagggtg
 240

gtccttaciaa tgaccaacgt ggacccagcg gacacagcca cctattactg tacacacgag
 300

caatactatt atgatactag tgggtcagcca tactactttg acttctgggg ccagggcacc
 360

ctgggtcacccg tctcctcagg cgggtggtgga tcaggcggcg gaggatctgg cggaggtggc
420

agcgggtggtg gaggcagtaa catccagggtg acccagtctc catcctccct gtctgcatct
480

gtaggagaca gagtcacccat gacttgccgg gcgagtcagg acattaggaa gaatttaa
540

tggtatcagc aaaaaccagg gaaagcccct aaggtcctga tctacgatgc atccgatttg
600

gaaacaggga tcccatcaag gttcagtgga agtggatctg ggacagattt tctcctcacc
660

atcagcagcc tgcagcctga agatattgca acatactact gtcaacagtc tgattattta
720

ccgctcactt tcggcggagg gaccaaagtg gatatacaaa
759

<210> 31
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone 15.150.24 Variant
<400> 31

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Thr Thr
20 25 30

Gly Glu Gly Val Gly Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

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Leu	Lys	Ser	Arg	Leu	Thr	Ile	Thr	Lys	Asp	Thr	Ser	Lys	Lys	Gln	Val
65					70					75					80
Val	Leu	Thr	Met	Thr	Asn	Val	Asp	Pro	Ala	Asp	Thr	Ala	Thr	Tyr	Tyr
				85					90					95	
Cys	Thr	His	Glu	Gln	Tyr	Tyr	Tyr	Asp	Thr	Ser	Gly	Gln	Pro	Tyr	Tyr
			100					105					110		
Phe	Asp	Phe	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly
		115					120					125			
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
	130					135					140				
Gly	Ser	Asn	Ile	Gln	Val	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser
145					150					155					160
Val	Gly	Asp	Arg	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Arg
				165					170					175	
Lys	Asn	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Val
			180					185					190		
Leu	Ile	Tyr	Asp	Ala	Ser	Asp	Leu	Glu	Thr	Gly	Ile	Pro	Ser	Arg	Phe
		195					200					205			
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Ile	Leu	Thr	Ile	Ser	Ser	Leu
	210					215					220				
Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Asp	Tyr	Leu
225					230					235					240
Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Asp	Ile	Lys			
				245					250						

<210> 32
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH CDR2

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> X = Asparagine or Threonine

<400> 32
 Gly Ser Thr Xaa Tyr Asn Pro Ser Leu
 1 5

<210> 33
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL CDR2

<220>
 <221> MISC_FEATURE
 <222> (3)..(4)
 <223> X3 = Asparagine or Threonine
 X4 = Threonine or Aspartic acid

<400> 33

Asp Ala Xaa Xaa Leu
 1 5

<210> 34
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 34

Genetastix.718.ST25

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Val Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Ser Ile Asn Trp Asn Asp Asp Lys Cys Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Pro Lys Asn Gln Val
65 70 75 80

Val Leu Ala Met Ser Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Ser
85 90 95

Cys Ala Leu Asp Met Pro Pro His Asp Ser Gly Pro Gln Ser Phe Asp
100 105 110

Ala Ser Asp Val Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 35
<211> 106
<212> PRT
<213> Homo sapiens

<400> 35

Ser Tyr Glu Leu Met Gln Leu Pro Ser Val Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Asp Asn Leu Gly Asp Lys Tyr Ala
20 25 30

Genetastix.718.ST25

Cys Trp Tyr Gln Gln Lys Pro Gly Arg Ser Pro Val Leu Val Ile Tyr
35 40 45

Gly Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Thr Ser Thr Ala Val
85 90 95

Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
100 105

<210> 36

<211> 126

<212> PRT

<213> Homo sapiens

<400> 36

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly His Asp
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile
35 40 45

Gly Phe Ile Phe Phe Asp Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Leu Ser Leu
65 70 75 80

Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala

Genetastix.718.ST25

85

90

95

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser
100 105 110

Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
115 120 125

<210> 37

<211> 104

<212> PRT

<213> Homo sapiens

<400> 37

Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Ser Ile Ser Cys Ser Gly Ser Ser Ser Asp Ile Gly Ser Asn
20 25 30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Phe Lys Ser Gly Thr Ser Ala Ser Leu Val Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Glu Ser Leu
85 90 95

Asn Gly Val Val Phe Gly Gly Gly
100

<210> 38

<211> 116

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<212> PRT
 <213> Homo sapiens

<400> 38

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Ser Trp Gly
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Ala Ser Phe Ser Gly Tyr
 20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Glu Ile Asn His Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Asp
 50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Thr Asn Gln Ile Ser Leu
 65 70 75 80

Lys Leu Thr Ser Met Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Thr Val Ala Gly Thr Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 39
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 39

Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly Asp
 1 5 10 15

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Lys Val Ser Ile Ser Cys Lys Ala Ser Arg Asp Val Asp Asp Asp Val
      20                      25                      30

Asn Trp Tyr Gln Gln Arg Pro Gly Glu Ala Pro Ile Phe Ile Ile Glu
      35                      40                      45

Asp Ala Thr Thr Leu Val Pro Gly Ile Ser Pro Arg Phe Ser Gly Ser
      50                      55                      60

Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Asp Ser Glu
65      70                      75                      80

Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Asn Phe Pro Leu Thr
      85                      90                      95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
      100                      105

<210> 40
<211> 126
<212> PRT
<213> Homo sapiens

<400> 40

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1      5                      10                      15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Thr Thr
      20                      25                      30

Gly Glu Gly Val Gly Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu
      35                      40                      45

Trp Leu Ala Leu Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser
      50                      55                      60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Lys Gln Val

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Genetastix.718.ST25

65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Thr His Glu Gln Tyr Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr
100 105 110

Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 41
<211> 107
<212> PRT
<213> Homo sapiens
<400> 41

Asn Ile Gln Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
5 10 15

Asp Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asp Ile Arg Lys Asn
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Asp Ala Ser Asp Leu Glu Thr Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Tyr Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

<210> 42
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker Sequence

<400> 42

Gly Gly Gly Gly Ser
 1 5

<210> 43
 <211> 21
 <212> PRT
 <213> Homo sapiens

<400> 43

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser
 1 5 10 15

Asp Gly Met Asp Val
 20

<210> 44
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 44

Arg Thr Val Ala Gly Thr Ser Asp Tyr
 1 5

<210> 45
 <211> 17
 <212> PRT
 <213> Homo sapiens

<400> 45

His Glu Gln Tyr Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr Phe Asp
1 5 10 15

Phe

<210> 46
<211> 11
<212> PRT
<213> Homo sapiens

<400> 46

Ala Ala Trp Asp Glu Ser Leu Asn Gly Val Val
1 5 10

<210> 47
<211> 9
<212> PRT
<213> Homo sapiens

<400> 47

Leu Gln His Asp Asn Phe Pro Leu Thr
1 5

<210> 48
<211> 9
<212> PRT
<213> Homo sapiens

<400> 48

Gln Gln Ser Asp Tyr Leu Pro Leu Thr
1 5

<210> 49
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 49

ggagaattcg attatcaagt gtcaagtcca
30

<210> 50

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 50

cgcggtatcct tagagcggag gcaggaggcg g
31

<210> 51

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 51

ggagaattca ccagatctca aaaagaagg
29

<210> 52

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 52

cgcggtatcct tatatcttta atgtctggaa att
33

<210> 53

<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 53
caggaattct ttggcctgaa t
21

<210> 54
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 54
cgcgatcct cagcagtgcg tcatcccaag a
31